

- 50 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: COHEN, CHARLES M.
- (ii) TITLE OF INVENTION: TREATMENT OF MAMMALIAN MYOCARDIUM WITH MORPHOGENICALLY-TREATED MYOGENIC PRECURSOR CELLS
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: TESTA, HURWITZ & THIBEAULT, LLP
 - (B) STREET: 125 HIGH STREET
 - (C) CITY: BOSTON
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: TWOMEY, MICHAEL J
 - (B) REGISTRATION NUMBER: 38,349
 - (C) REFERENCE/DOCKET NUMBER: CRP-123
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617/248-7000
 - (B) TELEFAX: 617/248-7100

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: /label= Generic-Seq-7
/note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

- 51 -

```

Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa Xaa
1           5           10           15
Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
20           25           30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa
35           40           45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Pro
50           55           60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65           70           75           80
Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
85           90           95
Xaa

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /label= Generic-Seq-8
/note= "wherin each Xaa is independently selected
from a group of one or more specified amino acids
as defined in the specification."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
1           5           10           15
Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
20           25           30
Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
35           40           45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50           55           60
Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
65           70           75           80
Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val
85           90           95
Xaa Xaa Cys Xaa Cys Xaa
100

```

- 52 -

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /label= OPX
/note= "WHEREIN EACH XAA IS INDEPENDENTLY SELECTED
FROM A GROUP OF ONE OR MORE SPECIFIED AMINO ACIDS
AS DEFINED IN THE SPECIFICATION"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
1           5           10           15
Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
20           25           30
Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
35           40           45
Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro lys
50           55           60
Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
65           70           75           80
Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
85           90           95
Xaa Ala Cys Gly Cys His
100

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..139

- 53 -

(D) OTHER INFORMATION: /label= hOP1-MATURE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1           5           10           15
Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
20           25           30
Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35           40           45
Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
50           55           60
Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
65           70           75           80
Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
85           90           95
Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
100          105          110
Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
115          120          125
Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130          135

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MURIDAE
- (F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: /label= MOP1-MATURE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Ser Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys
1           5           10           15
Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser
20           25           30
Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
35           40           45

```

- 54 -

Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
 50 55 60
 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
 65 70 75 80
 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
 85 90 95
 Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
 100 105 110
 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
 115 120 125
 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 130 135

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: HOMO SAPIENS
 - (F) TISSUE TYPE: HIPPOCAMPUS
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..139
 - (D) OTHER INFORMATION: /label= HOP2-MATURE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu
 1 5 10 15
 Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser
 20 25 30
 His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln
 35 40 45
 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
 50 55 60
 Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn
 65 70 75 80
 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
 85 90 95
 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
 100 105 110
 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
 115 120 125

- 55 -

Arg Asn Met Val Val Lys Ala Cys Gly Cys His
 130 135

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MURIDAE
- (F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (E) LOCATION: 1..139
- (D) OTHER INFORMATION: /label= MOP2-MATURE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln	Pro	Lys	Lys	Thr	Asn	Glu	Leu	1	5	10	15
Pro	His	Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp	Asp	Gly	His	Gly	Ser	20	25	30	
Arg	Gly	Arg	Glu	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	35	40	45	
Asp	Leu	Gly	Trp	Leu	Asp	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	50	55	60	
Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	65	70	75	80
Ala	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu	Val	His	Leu	Met	Lys	Pro	85	90	95	
Asp	Val	Val	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Ser	Ala	Thr	100	105	110	
Ser	Val	Leu	Tyr	Tyr	Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg	Lys	His	115	120	125	
Arg	Asn	Met	Val	Val	Lys	Ala	Cys	Gly	Cys	His						130	135		

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 56 -

(vi) ORIGINAL SOURCE:

(A) ORGANISM: bovinae

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..101

(D) OTHER INFORMATION: /label= CBMP-2A-FX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
 1 5 10 15
 Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly
 20 25 30
 Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala
 50 55 60
 Lys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
 65 70 75 80
 Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu
 85 90 95
 Gly Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

(F) TISSUE TYPE: hippocampus

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..101

(D) OTHER INFORMATION: /label= CBMP-2B-FX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
 1 5 10 15
 Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly
 20 25 30
 Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
 35 40 45

- 57 -

Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala
 50 55 60
 Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
 65 70 75 80
 Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu
 85 90 95
 Gly Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: DROSOPHILA MELANOGASTER

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: /label= DPP-FX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asp
 1 5 10 15
 Asp Trp Ile Val Ala Pro Leu Gly Tyr Asp Ala Tyr Tyr Cys His Gly
 20 25 30
 Lys Cys Pro Phe Pro Leu Ala Asp His Phe Asn Ser Thr Asn His Ala
 35 40 45
 Val Val Gln Thr Leu Val Asn Asn Asn Asn Pro Gly Lys Val Pro Lys
 50 55 60
 Ala Cys Cys Val Pro Thr Gln Leu Asp Ser Val Ala Met Leu Tyr Leu
 65 70 75 80
 Asn Asp Gln Ser Thr Val Val Leu Lys Asn Tyr Gln Glu Met Thr Val
 85 90 95
 Val Gly Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 58 -

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: XENOPUS

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /label= VGL-FX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys Asp Val Gly Trp Gln
1      5      10      15
Asn Trp Val Ile Ala Pro Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly
20      25      30
Glu Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly Ser Asn His Ala
35      40      45
Ile Leu Gln Thr Leu Val His Ser Ile Glu Pro Glu Asp Ile Pro Leu
50      55      60
Pro Cys Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met Leu Phe Tyr
65      70      75      80
Asp Asn Asn Asp Asn Val Val Leu Arg His Tyr Glu Asn Met Ala Val
85      90      95
Asp Glu Cys Gly Cys Arg
100

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: MURIDAE

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /label= VGR-1-FX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln Asp Val Gly Trp Gln
1      5      10      15
Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
20      25      30
Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
35      40      45

```

- 59 -

Ile Val Gln Thr Leu Val His Val Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Val Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: brain
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (E) LOCATION: 1..106
 - (D) OTHER INFORMATION: /note= "GDF-1 (fx)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp His
 1 5 10 15
 Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln Gly
 20 25 30
 Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro Ala
 35 40 45
 Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro Gly
 50 55 60
 Ala Ala Asp Leu Pro Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser
 65 70 75 80
 Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val Leu Arg Gln Tyr Glu
 85 90 95
 Asp Met Val Val Asp Glu Cys Gly Cys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids

- 60 -

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys Xaa Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1922 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HOMO SAPIENS
 (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 49..1341
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
 /product= "OP1"
 /evidence= EXPERIMENTAL
 /standard_name= "OP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGTGGGGGCC CGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG	57
	Met His Val
	1
CGC TCA CTG CCA GGT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA	105
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala	
5 10 15	
CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC	153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn	
20 25 30 35	
GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG	201
Glu Val His Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg	
40 45 50	
CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC	249
Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg	
55 60 65	

- 61 -

CCG CCG CCG CAC CTC CAG GCG AAG CAC AAC TCG GCA CCC ATG TTT ATG	297
Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met	
70 75 80	
CTG GAC CTC TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GCG CCC GCG	345
Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly	
85 90 95	
GCG CAG GCG TTC TCG TAC CCG TAC AAG GCG CTC TTC AGT ACC CAG GCG	393
Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly	
100 105 110 115	
CCC CTT CTC GCG AGC CTC CAA GAT AGC CAT TTC CTC ACC GAC GCG GAC	441
Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp	
120 125 130	
ATG CTC ATG AGC TTC CTC AAC CTC GTG GAA CAT GAC AAG GAA TTC CTC	489
Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe	
135 140 145	
CAC CCA CCG TAC CAC CAT CGA GAG TTC CCG TTT GAT CTT TCG AAG ATC	537
His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile	
150 155 160	
CCA GAA GCG GAA GGT GTC ACG GCA GCG GAA TTC CCG ATC TAC AAG GAC	585
Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
165 170 175	
TAC ATC CCG GAA CCG TTC GAC AAT GAG ACG TTC CCG AIC AGT GTT TAT	633
Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr	
180 185 190 195	
CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTC CTC	681
Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu	
200 205 210	
GAC AGC GGT ACC CTC TGG GCG TCG GAG GAG GCG TGG TTG GTG TTT GAC	729
Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp	
215 220 225	
ATG ACA GCG ACC AGC AAC CAC TGG GTG GTC AAT CCG CCG CAC AAC CTC	777
Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu	
230 235 240	
GCG CTC CAG CTC TCG GTG GAG ACG CTC GAT GCG CAG ACC ATC AAC CCG	825
Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro	
245 250 255	
AAG TTG GCG GCG CTC ATT GGG CCG CAC GCG CCG CAG AAC AAG CAG CCG	873
Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro	
260 265 270 275	
TTT ATG GTG CTT TTC TTC AAG GCG ACG GAG GTC CAC TTC CCG AGC ATC	921
Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile	
280 285 290	
CGG TCG AAG GCG AGC AAA CAG CGC ACG CAG AAC CCG TCG AAG ACG CCG	969
Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro	
295 300 305	
AAG AAC CAG GAA GCC CTC CCG ATG GCG AAC GTG GCA GAG AAC AGC AGC	1017
Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser	
310 315 320	

- 62 -

AGC GAG CAG AGG CAG GGC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe 325 330 335	1265
CGA GAG CTG GGC TGG CAG GAG TGG ATC ATC GCG CCT GAA GGC TAC GCC Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala 340 345 350 355	1273
GCC TAA TAC TGT GAG GGG GAG TGT GGC TTC CCT CTG AAC TCG TAC ATG Ala Tyr Tyr Cys Glu Gly Gln Cys Ala Phe Pro Leu Asn Ser Tyr Met 360 365 370	1281
AAC GGC ACC AAC CAC GGC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn 375 380 385	1289
CCG GAA ACG GTG GCG AAG CCC TGC TGT GCG CCC ACG CAG CTG AAT GCC Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala 390 395 400	1297
ATC TCG GTC CTC TAC TTC CAT GAG AGC TCG AAC GTC ATC CTG AAG AAA Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys 405 410 415	1305
TAC AGA AAC ATG GTC GTC CGG GCC TGT GGC TCG CAC TAGCTCCTCC Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His 420 425 430	1351
GAGAATTTCAG ACCCTTTGCGG GCGAAGTTTT TTTGGATCCT CCATTGCTCG CCTTGGCCAG GAACCAGCAG ACCAACTGCC TTTTGTGAGA CTTTCCCTTC CCTATCCCCA ACTTTAAAGG TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGCTTTTGG ATCAGTTTTT CAGTGGCAGC ATCCAAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAAAC TAGCAGGAAA AAAAAACAAC GCATAAAGAA AAATGGCGCG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT CGTTTTCAGA GGTAATTATG AGCGCTTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG GGCTGGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC CTGTAATAAA TGTACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A	1411 1471 1531 1591 1651 1711 1771 1822

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	His	Val	Arg	Ser	Leu	Arg	Ala	Ala	Ala	Pro	His	Ser	Phe	Val	Ala
1				5					10					15	
Leu	Trp	Ala	Pro	Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser
		20						25					30		

- 63 -

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
 35 40 45
 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
 50 55 60
 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80
 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
 85 90 95
 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
 100 105 110
 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
 115 120 125
 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
 130 135 140
 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
 145 150 155 160
 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
 165 170 175
 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
 180 185 190
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
 195 200 205
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 210 215 220
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365

- 64 -

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (E) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MURIDAE
- (F) TISSUE TYPE: EMERYO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 104..1393
- (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
 /product= "MOPI"
 /note= "MOPI (CDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGCAGCAAG TGACCTGGGG TCCTGGACCG CTGCCCTGCC CCCTCCGCTG CCACTG3GGG 60

CGGCGCGGGG CCGGTGCCCC GGATCGCGCG TAGAGCCCGG GCG ATG CAC GTG CGG 115
 Met His Val Arg
 1

TCG CTG CGC GCT GCG GCG CCA CAC AGC TTC GTG GCG CTC TGG GCG CCT 163
 Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro
 5 10 15 20

CTG TTC TTG CTG CGC TCC GCC CTG GCG GAT TTC AGC CTC GAC AAC GAG 211
 Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu
 25 30 35

GTG CAC TCC AGC TTC ATC CAC CGG CGC CTC CCC AGC CAG GAG CGG CGG 259
 Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg
 40 45 50

GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CGG 307
 Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro
 55 60 65

CGC CGG CAC CTC CAG GGA AAG CAT AAT TCG GCG CCC ATG TTC ATG TTG 355

- 65 -

Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	Met	Phe	Met	Leu	
70						75					80					
GAC	CTG	TAC	AAC	GCC	ATG	GAG	GTG	GAG	GAG	AGC	GGG	CCG	GAC	GGG	CAG	403
Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Ser	Gly	Pro	Asp	Gly	Gln	
85					90					95					100	
GGG	TTC	TCT	TAC	CCC	TAC	AAG	GCC	CTC	TTC	AGT	ACC	CAG	GGG	CCC	CCT	451
Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	Pro	Pro	
				105					110					115		
TTA	GCC	AGC	CTG	CAG	GAC	AGC	CAT	TTC	CTC	ACT	GAC	GGC	GAC	ATG	GTG	499
Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	Met	Val	
			120					125				130				
ATG	AGC	TTC	GTG	AAC	CTA	GTG	GAA	CAT	GAC	AAA	GAA	TTC	TTC	CAC	CCT	547
Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	His	Pro	
	135					140						145				
CGA	TAC	CAC	CAT	CCG	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	CCC	GAG	595
Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	Pro	Glu	
150						155					160					
GGC	GAA	CGG	GTG	ACC	GCA	GCC	GAA	TTC	AGG	ATC	TAT	AAG	GAC	TAC	ATC	643
Gly	Glu	Arg	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	Tyr	Ile	
165					170					175				180		
CGG	GAG	CGA	TTT	GAC	AAC	GAG	ACC	TTC	CAG	ATC	ACA	CTC	TAT	CAG	GTG	691
Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Gln	Ile	Thr	Val	Tyr	Gln	Val	
				185				190						195		
CTC	CAG	GAG	CAC	TCA	GGC	AGG	GAG	TGG	GAC	CTC	TTC	TTG	CTG	GAC	ACC	739
Leu	Gln	Glu	His	Ser	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	Asp	Ser	
			200					205					210			
CGC	ACC	ATC	TGG	GCT	TCT	GAG	GAG	GSC	TGG	TTG	GTG	TTT	GAT	ATC	ACA	787
Arg	Thr	Ile	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	Ile	Thr	
	215						220					225				
GCC	ACC	AGT	AAC	CAC	TGG	GTG	GTC	AAC	CCT	CGG	CAC	AAC	CTG	GGC	TTA	835
Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	Gly	Leu	
	230					235					240					
CAG	CTC	TCT	GTG	GAG	ACC	CTG	GAT	GCG	CAG	AGC	ATC	AAC	TCC	AAG	TTG	883
Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	Lys	Leu	
245					250					255				260		
GCA	GGC	CTG	ATT	GGA	CGG	CAT	GGA	CCC	CAG	AAC	AAG	CAA	CCC	TTC	ATG	931
Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	Phe	Met	
				265				270						275		
GTG	GGC	TTC	TTC	AAG	GCC	ACG	GAA	GTG	CAT	CTC	CGT	AGT	ATC	CGG	TCC	979
Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Leu	Arg	Ser	Ile	Arg	Ser	
			280					285					290			
ACG	GGG	GGC	AAG	CAG	CGC	AGC	CAG	AAT	CGC	TCC	AAG	ACG	CCA	AAG	AAC	1027
Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	
	295						300					305				
CAA	GAG	GCC	CTG	AGG	ATG	GCC	AAT	GTG	GCA	GAA	AAC	AGT	AGC	AGT	GAC	1075
Gln	Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala	Glu	Asn	Ser	Ser	Ser	Asp	
310						315					320					

- 66 -

CAG AGG CAG ACC TGG AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAC 1123
 Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp
 315 330 335 340
 CTT GGC TGG CAG GAG TGG ATC ATT GCA CCT GAA GGC TAT GCT GGC TAC 1171
 Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr
 345 350 355
 TAC TGT CAG GGA GAG TGG GGC TTC CTT CTG AAC TCC TAC ATG AAC GGC 1219
 Tyr Cys Glu Gly Gln Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala
 360 365 370
 ACC AAC CAC GGC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC 1267
 Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp
 375 380 385
 ACA GTA CCC AAG CCG TGG TGT GCG CCC ACC CAG CTC AAC CCC ATC TCT 1315
 Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser
 390 395 400
 GTC CTC TAC TTC GAC GAG AGC TGT AAT GTC ATC CTC AAG AAG TAC AGA 1363
 Val Leu Tyr Phe Asp Asn Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg
 405 410 415 420
 AAC ATG CTG CTC CGG CCG TGT GGC TGC CAC TACCTCTTCC TGAGACCCCTG 1413
 Asn Met Val Val Arg Ala Cys Gly Cys His
 425 430
 ACCTTTGCGG GGGCACACCT TCCAAAATCT TCGATGTCT ACCATCTAAG TCTCTCAGTG 1473
 CCCACCTTGG CAGAGGAGAA AGACCAACCT CTCCTGAGCC TTCCTCAGC TCCCAACCGG 1533
 AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCCTC CTTTCTTTCT 1593
 GGCACGTGAG GGATAAGATC CTACAGCTA CCACAACAAA CGCTTAAGAG CAGGAAAAAT 1653
 GTCTGCCAAG AAAGTGTCCA GTGTCCACAT GGCCTCTGCG GGTCTGAGT TTTGAGGAGT 1713
 AATCGCAAG CTCCTTCAGC TCCACACAGAA GGAAGGGCTT AGCCAGGGTG GGCCTGCGCG 1773
 TCTGTGTTGA AGAGAAACCA AGCAGAGCC ACTGTAATGA TATGTACAA TAAACCCAT 1833
 GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC 1873

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1 5 10 15
 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
 20 25 30
 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser

- 67 -

35	40	45
Gln Glu Arg Arg Glu Met	Gln Arg Glu Ile Leu Ser	Ile Leu Gly Leu
50	55	60
Pro His Arg Pro Arg Pro His	Leu Gln Gly Lys His Asn	Ser Ala Pro
65	70	75
Met Phe Met Leu Asp Leu Tyr	Asn Ala Met Ala Val Glu Glu	Ser Gly
85	90	95
Pro Asp Gly Gln Gly Phe Ser Tyr	Pro Tyr Lys Ala Val Phe	Ser Thr
100	105	110
Gln Gly Pro Pro Leu Ala Ser	Leu Gln Asp Ser His Phe	Leu Thr Asp
115	120	125
Ala Asp Met Val Met Ser Phe	Val Asn Leu Val Glu His	Asp Lys Glu
130	135	140
Phe Phe His Pro Arg Tyr His	His Arg Glu Phe Arg Phe	Asp Leu Ser
145	150	155
Lys Ile Pro Glu Gly Glu Arg	Val Thr Ala Ala Glu Phe	Arg Ile Tyr
165	170	175
Lys Asp Tyr Ile Arg Glu Arg	Phe Asp Asn Glu Thr Phe	Gln Ile Thr
180	185	190
Val Tyr Gln Val Leu Gln Glu	His Ser Gly Arg Glu Ser	Asp Leu Phe
195	200	205
Leu Leu Asp Ser Arg Thr Ile	Trp Ala Ser Glu Glu Gly	Trp Leu Val
210	215	220
Phe Asp Ile Thr Ala Thr Ser	Asn His Trp Val Val Asn	Pro Arg His
225	230	235
Asn Leu Gly Leu Gln Leu Ser	Val Glu Thr Leu Asp Gly	Gln Ser Ile
245	250	255
Asn Pro Lys Leu Ala Gly Leu	Ile Gly Arg His Gly Pro	Gln Asn Lys
260	265	270
Gln Pro Phe Met Val Ala Phe	Phe Lys Ala Thr Glu Val	His Leu Arg
275	280	285
Ser Ile Arg Ser Thr Gly Gly	Lys Gln Arg Ser Gln Asn	Arg Ser Lys
290	295	300
Thr Pro Lys Asn Gln Glu Ala	Leu Arg Met Ala Ser Val	Ala Glu Asn
305	310	315
Ser Ser Ser Asp Gln Arg Gln	Ala Cys Lys Lys His Glu	Leu Tyr Val
325	330	335
Ser Phe Arg Asp Leu Gly Trp	Gln Asp Trp Ile Ile Ala	Pro Glu Gly
340	345	350
Tyr Ala Ala Tyr Tyr Cys Glu	Gly Glu Cys Ala Phe Pro	Leu Asn Ser
355	360	365
Tyr Met Asn Ala Thr Asn His	Ala Ile Val Gln Thr Leu	Val His Phe

- 68 -

370 375 380
 Ile Asn Pro Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu
 385 390 395 400
 Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu
 405 410 415
 Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 490..1696
- (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
 /product= "hOP2-PP"
 /note= "hOP2 (cDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGC3CCGGCA BAC3AGGAGT G3CT3GAGGA GCTGTGTTT3 GAGCAGGAGG TBGCACG3CA 60
 GGGCT3GAGG BCTCCCTAT3 AGT3GGGGAG ACGGCCAG3 AGGGGCTGGA GCAACAG3TC 120
 CCACA3CGCA CCAAGGGGT3 GCTGCAGGAG CTGCCCCAT3 GGGCCTGCGC TGCTCGGACC 180
 GCGGCCACAG CCGGACTGGC GGGTACGGGG GCGACAGAG3 CATTTGGCCGA GAGTCCCAST 240
 CGCAGAGTA G1CCCCGGCT CGAG3CGGTG GCSTCCGGT CTTCTCCCTC CAGGAGCCAG 300
 GACAGGTGTC G3GGGGCGGG GCTCCAGGGA CC3CGCCTGA GGC3GGTGT3 CCGCCCGTCC 360
 CGCCCGGCCC CGCC3CGGC CGCCCGCCGA GGCAGCCTC CTTGCCGTGG GGGCGTCCCC 420
 AGGCCTTGGG TGGG3CGGG AGCCSATGGC CGCC3CTGA G3CCCCAG3 TBAGCCCCCC 480
 CG3CCTGCC AT3 ACC GGG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTC 528
 Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu
 1 5 10
 GGG CTA TGC GCG CTC GGC GGG GGC GGC CCC GGG CTC CGA CCG CCG CCG 576
 Ala Leu Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro
 15 20 25
 GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC CTG CAG 624
 Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Gln Arg Arg Asp Val Gln
 30 35 40 45

CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC GGC	672
Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg	
50 55 60	
GCG CCA CCC GCG GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG	720
Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met	
65 70 75	
CTG GAC CTG TAC CAC GGC ATG GCG GGC GAC GAC GAC GAG GAC GGC GCG	768
Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala	
80 85 90	
CCC GCG GAG CCG CGC CTG GCG GCG GCG GAC CTG GTC ATG ACC TTC ATT	816
Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val	
95 100 105	
AAC ATG CTG GAG CGA GAC CCG GCG CTG GCG GAC CAG GAG CTC CAT TGG	864
Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp	
110 115 120 125	
AAG GAG TTC CCG TTT GAC CTG ACC CAG ATC CCG GCT GCG GAG GCG CTC	912
Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val	
130 135 140	
ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAT CTC CTC	960
Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu	
145 150 155	
AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG CTG CTC CAG GAG CAG TCC	1008
Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser	
160 165 170	
AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACC CTC CGA GGT	1056
Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala	
175 180 185	
GGA GAC GAG GCG TGG CTG GTG CTG GAT GTC ACA GCA GCG AGT GAC TGC	1104
Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys	
190 195 200 205	
TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTG CCG CTC TAT GTG GAG	1152
Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu	
210 215 220	
ACT GAG GAC GCG CAC AGC GTG GAT CCT GGC CTG SCC GGC CTG CTG GGT	1200
Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly	
225 230 235	
CAA CCG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG	1248
Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg	
240 245 250	
GCC AGT CCG AGT CCC ATC CCG ACC CCT CCG GCA GTG AGG CCA CTG AGG	1296
Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg	
255 260 265	
AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCT AAC CCA CTC	1344
Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu	
270 275 280 285	
CCA GCG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CCG CAG GTC TGC	1392
Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys	
290 295 300	

- 70 -

CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG CTG GAC 1440
 Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp
 305 310 315

TGG GTC ATC GCT CCC CAA GGC TAC TCG GCC TAT TAC TGT GAG GGG GAG 1488
 Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu
 320 325 330

TGC TCC TTC CCA CTG GAC TCC TGC ATG AAT GCG ACC AAC CAC GCC ATC 1536
 Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile
 335 340 345

CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG 1584
 Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala
 350 355 360 365

TGC TGT GCA GCG ACC AAG CTG AGC GCG ACC TCT GTG CTC TAC TAT GAC 1632
 Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
 370 375 380

AGC AGC AAC AAC CTC ATC CTG CGT AAA CAC GCG AAC ATG GTG GTC AAG 1680
 Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys
 385 390 395

GCC TGC GCG TCC CAC T GAGTCAGCCC GCCCAGCCCT ACTGCAG 1723
 Ala Cys Gly Cys His
 400

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1 5 10 15

Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro Gly Cys Pro
 20 25 30

Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln Arg Glu Ile
 35 40 45

Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Pro Pro
 50 55 60

Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu
 65 70 75 80

Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala Pro Ala Glu
 85 90 95

Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val
 100 105 110

Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp Lys Glu Phe

- 71 -

115	120	125
Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala 130 135 140		
Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu Asn Arg Thr 145 150 155 160		
Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser Asn Arg Glu 165 170 175		
Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp Glu 180 185 190		
Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys Trp Leu Leu 195 200 205		
Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp 210 215 220		
Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala 225 230 235 240		
Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro 245 250 255		
Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg Gln 260 265 270		
Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu Pro Gly Ile 275 280 285		
Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His 290 295 300		
Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile 305 310 315 320		
Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe 325 330 335		
Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser 340 345 350		
Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala 355 360 365		
Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn 370 375 380		
Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly 385 390 395 400		
Cys His		

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1926 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 72 -

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MURIDAE
(F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 93..1289
(D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "mOP1-pp"
/note= "MOI2 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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GCCAGGACAA GGTGCTCCCT CTGGTCTCTCC CCGTCTGCGG TCAGCCGAGC CCGACCAAGCT      60
ACCACTGGAT GGGGCTCGGG TGAAAGTCCG AG ATG GCT ATG CGT CCC GGG CCA      113
                                     Met Ala Met Arg Pro Gly Pro
                                     1           5
CTC TGG CTA TTG GGC GTT GCT CTC TGC GCG CTG GGA GGG GGC CAC GCT      161
Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly Gly His Gly
          10          15          20
CCG CGT CCC CCC TAC ACC TGT CCC CAG CGT GGC CTC GGA GCG CGC CAG      209
Pro Arg Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu
          25          30          35
CGC CGC GAC ATG CAG CGT GAA ATC CTC GCG CTC CTC GGG CTA CCC GGA      257
Arg Arg Asp Met Gln Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly
          40          45          50          55
CGG CCT CGA CCC CGT GCA CAA CCC GCG GCT GCG CGG CAG CCA GGG TCC      305
Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala Ala Arg Gln Pro Ala Ser
          60          65          70
GCG CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG ACC GAT GAC GAC      353
Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr Asp Asp
          75          80          85
GAC GGC GGG CCA CCA CAG GCT CAC TTA GGC CGT GCC GAC CTG GTC ATG      401
Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp Leu Val Met
          90          95          100
AGC TTC GTC AAC ATG GTG GAA CGC GAC CGT ACC CTC GGC TAC CAG GAG      449
Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly Tyr Gln Glu
          105          110          115
CCA CAC TGG AAG GAA TTC CAC TTT GAC CTA ACC CAG ATC CCT GCT GGG      497
Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile Pro Ala Gly
          120          125          130          135
GAG GCT GTC ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA CCC AGC ACC      545
Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu Pro Ser Thr
          140          145          150
CAC CGG CTC AAC ACA ACC CTC CAC ATC AGC ATG TTC GAA GTC GTC CAA      593
His Pro Leu Asn Thr Thr Leu His Ile Ser Met Phe Glu Val Val Gln
          155          160          165
GAG CAC TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACC      641
Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr

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- 73 -

170	175	180	
CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG CTC GAC ATC ACA GCA GCG Leu Arg Ser Gly Asp Gln Gly Trp Leu Val Leu Asp Ile Thr Ala Ala 185 190 195			689
AGT GAC CGA TGG CTG CTG AAC CAT CAC AAG GAC CTG GCA CTC GGG CTC Ser Asp Arg Trp Leu Leu Asn His His Lys Asp Leu Gly Leu Arg Leu 200 205 210 215			737
TAT GTG GAA AGC GGG GAT GGG CAC ACC ATG CAT CCT GGC CTG GCT GGT Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp Pro Gly Leu Ala Gly 220 225 230			785
CTG CTT GGA CGA CAA GCA CCA GGC TAC AAA CAG CCT TTC ATG GTA ACC Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln Pro Phe Met Val Thr 235 240 245			833
TTC TTT AGG GGC AGC CAG AGT CCT GTG GGG GGC CCT CGG GCA GCG AGA Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro Arg Ala Ala Arg 250 255 260			881
CCA CTG AAG AGG AGG CAG CCA AAG AAA AGC AAC GAG CTT CGG CAC CCC Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu Pro His Pro 265 270 275			929
AAC AAA CTC GCA GGG ATC TTT GAT GAT GGC CAC GGT TCC CGG GGC AGA Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser Arg Gly Arg 280 285 290 295			977
GAG GTT TGC GGC AGG CAT GAG CTC TAC GTC ACC TTC CST GAC CTT GGC Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly 300 305 310			1025
TGG CTG GAT TGG GTC ATC GCC CCC CAG GGC TAC TCT GGC TAT TAC TGT Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys 315 320 325			1073
GAG GGG GAG TGT GGT TTC CCA CTG GAC TCC TGT ATG AAC GGC ACC AAC Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn 330 335 340			1121
CAT GGC ATC TTG CAG TCT CTG GTG CAC CTG ATG AAG CCA GAT GTT GTC His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asp Val Val 345 350 355			1169
CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG AGT GGC ACC TCT GTG CTG Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu 360 365 370 375			1217
TAC TAT GAC AGC AGC AAC AAT GTC ATC CTG CTT AAA CAC CGT AAC ATG Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met 380 385 390			1265
GTG GTC AAG GGC TGT GGC TGC CAC TTAGGGGCGG CCCAGCATCC TCCTTCTACT Val Val Lys Ala Cys Gly Cys His 395			1319
ACCTTACCAT CTGGCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT TATCATAGCT 1379			
CAGACAGGGG CAATGGGAGG CCCTTCACTT CCCCTGGCCA CTTCTGCTA AAATTCTGGT 1439			
CTTCCCAGT TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGGC CTCTCCATCC 1499			

- 74 -

TCCTACCCCA AGCATAGACT GAATGCACAC AGCATCCCAG AGCTATGCTA ACTGAGAGGT 1589
 CTGGGGSTCAG CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC CTCAGGCCAC 1619
 AATGGGAAAT TTTGGATGCT TTAAGAAGGC CCTGGAATTC TAAACTAGAT GATCTGGGCT 1679
 CTCTGCACCA TTCATTGTGG CAGTTGGGAC ATTTTITAGGT ATAACAGACA CATACACTTA 1739
 GATCAATGCA TGGGTGTACT CTTTGAAATC AGACCTAGGT TSTTAGAAAA AGAATCAGAG 1799
 CCAGSTATAG CGGTGCATGT CATTAATGTC AGCCTAAAG AGACAGAGAC AGGAGAATCT 1859
 CTGTGAGTTC AAGGCCACAT AGAAAGAGCC TSTCTGGGGA GCAGGAAAAA AAAAAAAAC 1919
 GGAATTC 1926

(x) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- A) LENGTH: 399 amino acids
- B) TYPE: amino acid
- C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ala Met Arg Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1 5 10 15
 Ala Leu Gly Gly Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln
 20 25 30
 Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu
 35 40 45
 Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala
 50 55 60
 Ala Ala Arg Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr
 65 70 75 80
 His Ala Met Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu
 85 90 95
 Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp
 100 105 110
 Arg Thr Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp
 115 120 125
 Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg
 130 135 140
 Ile Tyr Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile
 145 150 155 160
 Ser Met Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu
 165 170 175
 Phe Phe Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu

- 75 -

180	185	190
Val Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His 195 200 205		
Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser 210 215 220		
Met Asp Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser 225 230 235 240		
Arg Gln Pro Phe Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val 245 250 255		
Arg Ala Pro Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys 260 265 270		
Thr Asn Glu Leu Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp 275 280 285		
Gly His Gly Ser Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr 290 295 300		
Val Ser Phe Arg Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln 305 310 315 320		
Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp 325 330 335		
Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His 340 345 350		
Leu Met Lys Pro Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys 355 360 365		
Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile 370 375 380		
Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His 385 390 395		

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1368
- (D) OTHER INFORMATION: /label= "60A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG TCG GGA CTG CGA AAC ACC TCG GAG GCC GTT GCA GTG CTC GCC TCC
Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser
1 5 10 15

CTG GGA CTC GGA ATG GTT CTG CTC ATG TTC GTG GGG ACC AAG CCG CCG Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro 20 25 30	96
GCC GTT GAG GCC ACC CAG TCG GGG ATT TAC ATA GAC AAC GGC AAG GAC Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp 35 40 45	144
CAG AAG ATT ATG CAC AGA GTG CTG ACC GAG GAC GAC AAG CTG GAC CTC Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val 50 55 60	192
TCG TAC GAG ATC CTC GAG TTC CTG GGC ATC GTC GAA CCG CCG ACG CAC Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His 65 70 75 80	240
CTG AGC ACC CAC CAG TTG TCG CTG AGG AAG TCG GCT CCG AAG TTC CTG Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu 85 90 95	288
CTG GAC CTC TAC CAC CGC ATC ACC GCG GAG GAG GGT CTC ACC GAT CAG Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln 100 105 110	336
GAT GAG GAG GAC GAC TAC GAA CGC GGT CAT CCG TCC AGG AGG ACC GCC Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala 115 120 125	384
GAC CTC GAG GAG GAT GAG GGC GAG CAG CAG AAG AAC TTC ATT ACC GAC Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp 130 135 140	432
CTG GAC AAG CCG GCC ATC GAC GAG AGC GAC ATC ATC ATG ACC TTC CTG Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu 145 150 155 160	480
AAC AAG CGC CAC CAC AAT GTG GAC GAA CTG CGT CAC GAG CAC GGC CGT Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg 165 170 175	528
CGC CTG TGG TTC GAC GTC TCC AAC GTG CCC AAC GAC AAC TAC CTG GTG Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val 180 185 190	576
ATG GCC GAG CTG CGC ATC TAT CAG AAC GCC AAC GAG GGC AAG TGG CTG Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu 195 200 205	624
ATC GCC AAC AGG GAG TTC ACC ATC AGG GTA TAT GCC ATT GGC ACC GGC Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly 210 215 220	672
ACC CTG GGC CAG CAC ACC ATG GAG CCG CTG TCC TCG GTG AAC ACC ACC Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr 225 230 235 240	720
GGG GAC TAC GTG GGC TGG TTG GAG CTC AAC GTG ACC GAG GGC CTG CAC Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His 245 250 255	768
GAG TGG CTG GTC AAG TGG AAG GAC AAT CAT GGC ATC TAC ATT GGA GCA Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala 260 265 270 275 280 285 290 295	816

- 77 -

260	265	270	
CAC GGT GTC AAC CGA CCC GAC CGC GAG GTG AAG CTG GAC CAC ATT GGA His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly 275 280 285			864
CTG ATC CAC CAC AAG CTC GAC GAC GAG TTC CAG CCC TTC ATG ATC GGC Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly 290 295 300			912
TTC TTC CCC GGA CCG GAG CTG ATT AAG GCG ACG GTC CAC AGC AGC CAC Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His 305 310 315 320			960
CAC AGC AGC AAG CGA AGC CCC AGC CAT CCA CGC AAG CGC AAG AAG TCG His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser 325 330 335			1008
GTG TCG CCC AAC AAC CTC CCG CTG CTG GAA CCG ATG GAG AGC ACG CGC Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg 340 345 350			1056
AGC TGT CAG ATG CAG ACC CTG TAC ATA GAC TTC AAG GAT CTG GGC TGG Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp 355 360 365			1104
CAT GAC TGG ATC ATC GCA CCA GAG GGC TAT GGC GGC TTC TAC TGC AGC His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser 370 375 380			1152
GGC GAG TGG AAT TTC CCG CTC AAT GCG CAC ATG AAC GGC ACG AAC CAT Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His 385 390 395 400			1200
GCG ATC GTC CAG ACC CTG GTC CAC CTG CTG GAG CCC AAG AAG GTG CCC Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro 405 410 415			1248
AAG CCG TGC TGC GGT CCG ACC AGG CTG GGA GGA CTA CCG GTT CTG TAC Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr 420 425 430			1296
CAC CTG AAC GAC GAG AAT GTG AAC CTG AAA AAG TAT AGA AAC ATG ATT His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile 435 440 445			1344
GTG AAA TCC TGC GGG TGC CAT TGA Val Lys Ser Cys Gly Cys His 450 455			1368

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser

- 78 -

1	5	10	15
Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro	20	25	30
Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp	35	40	45
Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val	50	55	60
Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His	65	70	75
Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu	85	90	95
Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln	100	105	110
Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala	115	120	125
Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp	130	135	140
Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu	145	150	155
Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg	165	170	175
Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val	180	185	190
Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu	195	200	205
Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly	210	215	220
Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr	225	230	235
Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His	245	250	255
Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala	260	265	270
His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly	275	280	285
Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly	290	295	300
Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His	305	310	315
His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser	325	330	335
Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg			

- 79 -

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          340          345          350
Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp
          355          360          365
His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser
          370          375          380
Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
          385          390          395          400
Ala Ile Val Ser Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro
          405          410          415
Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr
          420          425          430
His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile
          435          440          445
Val Lys Ser Cys Gly Cys His
          450          455

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(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1674 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 69..1268
- (D) OTHER INFORMATION: /note= "mOP3-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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GGATCCGCGG CGCTGTCCCA TCCTTGTCGT CGAGGCGTGG CTGGATGCGA GTCCGCTAAA      60
CGTCCGAG ATG GCT GCG CGT CCG GGA CTC CTA TGG CTA CTG GGC CTG GGT      110
      1      5      10
      Met Ala Ala Arg Pro Gly Leu Leu Trp Leu Leu Gly Leu Ala
CTG TGC GTG TTG GGC GGC GGT CAC CTC TGG CAT CCC CCG CAC GTC TTT      158
Leu Cys Val Leu Gly Gly Gly His Leu Ser His Pro Pro His Val Phe
      15      20      25      30
CCC CAG CGT CGA CTA GGA GTA GGC GAG CCC GGC GAC ATG CAG CGC GAG      206
Pro Gln Arg Arg Leu Gly Val Arg Glu Pro Arg Asp Met Gln Arg Glu
      35      40      45
ATT CGG GAG GTG CTG GGG CTA GCC GGG CGG CCC CGA TCC CGA GCA CGG      254
Ile Arg Glu Val Leu Gly Leu Ala Gly Arg Pro Arg Ser Arg Ala Pro
      50      55      60
GTC GGG GCT GCC CAG CAG CCA GCG TCT GCG CCC CTC TTT ATG TTG GAC      302
Val Gly Ala Ala Gln Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp

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- 80 -

65	70	75	
CTG TAC CCG GGC ATG ACG GAT GAC AGT GGC GGT GGG ACC CCG CAG CCT Leu Tyr Arg Ala Met Thr Asp Asp Ser Gly Gly Gly Thr Pro Gln Pro 80 85 90			350
CAC TTG GAC CCG GGT GAC CTG ATT ATG ACG TTT GTC AAC ATA GTG GAA His Leu Asp Arg Ala Asp Leu Ile Met Ser Phe Val Asn Ile Val Glu 95 100 105 110			398
CGC GAC CCG ACC CTG GGC TAC CAG GAG CCA CAC TGG AAG GAA TTC TAC Arg Asp Arg Thr Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His 115 120 125			446
TTT GAC CTA ACC CAG ATC CCG GGT GGC GAG GGT GTC ACA GGT GGT CAG Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu 130 135 140			494
TTC CGG ATC TAC AAA GAA CCG AGT ACC CAC CCG CTC AAC ACA ACC CTC Phe Arg Ile Tyr Lys Glu Pro Ser Thr His Phe Leu Asn Thr Thr Leu 145 150 155			542
CAC ATC AGC ATG TTC GAA GTG CTC CAA GAG CAC TCC AAC AGG GAG TCT His Ile Ser Met Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser 160 165 170			590
GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA TTT GGG GAC GAG GGC Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly 175 180 185 190			638
TGG CTG GTG CTG GAC ATC ACA GCA GCC AGT GAC CGA TGG CTG CTG AAC Trp Leu Val Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn 195 200 205			686
CAT CAC AAG GAC CTA GGA CTC CGC CTC TAT GTG GAA ACC GAG GAT GGG His His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp Gly 210 215 220			734
CAC AGC ATA GAT CCG GGC CTA GGT GGT CTG CTT GGA CGA CAA GCA CCA His Ser Ile Asp Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro 225 230 235			782
CGC TCC AGA CAG CCG TTC ATG GTT GGT TTC TTC ACG GCC AAC CAG AGT Arg Ser Arg Gln Pro Phe Met Val Gly Phe Phe Arg Ala Asn Gln Ser 240 245 250			830
CCT GTG CGG GCG CCT CGA ACA GCA AGA CCA CTG AAG AAG AAG CAG CTA Pro Val Arg Ala Pro Arg Thr Ala Arg Pro Leu Lys Lys Lys Gln Leu 255 260 265 270			878
AAT CAA ATC AAC CAG CTG CCG CAC TCC AAC AAA CAC CTA GGA ATC CTT Asn Gln Ile Asn Gln Leu Pro His Ser Asn Lys His Leu Gly Ile Leu 275 280 285			926
GAT GAT GGC CAC GGT TCT CAC GGC AGA GAA GTT TGC CGC AGG CAT GAG Asp Asp Gly His Gly Ser His Gly Arg Glu Val Cys Arg Arg His Glu 290 295 300			974
CTC TAT GTC AGC TTC CCG GAC CTT GGC TGG CTG GAC TCT GTC ATT GGC Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Leu Asp Ser Val Ile Ala 305 310 315			1022
CCC CAG GGC TAC TCC GCC TAT TAC TGT GGT GGG GAG TGC ATC TAC CCA			1070

- 81 -

Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Ala Gly Glu Cys Ile Tyr Pro
 320 325 330

CTG AAC TCC TGT ATG AAC TCC ACC AAC CAC GCC ACT ATG CAG GCC CTG 1118
 Leu Asn Ser Cys Met Asn Ser Thr Asn His Ala Thr Met Gln Ala Leu
 335 340 345 350

GTA CAT CTG ATG AAG CCA GAT ATC ATC CCC AAG GTG TGC TGT GTG CCT 1166
 Val His Leu Met Lys Pro Asp Ile Ile Pro Lys Val Cys Cys Val Pro
 355 360 365

ACT GAG CTG AGT GCC ATT TCT CTG CTC TAC TAT GAT AGA AAC AAT AAT 1214
 Thr Gln Leu Ser Ala Ile Ser Leu Leu Tyr Tyr Asp Arg Asn Asn Asn
 370 375 380

GTC ATC CTG CCC AGG GAG CGC AAC ATG GTA GTC CAG GCC TGT GGC TGC 1262
 Val Ile Leu Arg Arg Glu Arg Asn Met Val Val Gln Ala Cys Gly Cys
 385 390 395

CAC TGAGTCCCTG CCCAACAGCC TGCTGCCATC CCATCTATCT AGTCAGGCCT 1315
 His
 400

CTCTTCCAAAG CCAGGAAACC AACAAAGAGG GAAAGCAATG CTTTCAACTC CATGTCCACA 1375

TTCACASTCT TGCCCTCTTC TGTTCTTTTT GCCAAGGCTG AGAAGATGGT CCTAGTIATA 1435

ACCCTGSTGA CCTCAGTAGC CCGATCTCTC ATCTCCCAAA ACTCCCAAT GCAGCCAGGG 1495

GCATCTATCT CTTTGGGAT TGGGCACAGA AGTCCAATTT ACCAAETTAT TCATGASTCA 1555

CTACTGCCCC AGCTTGSACT TGAACCTGGA ACACAGGGTA GAGTCAGGC TCTTCAGTAT 1615

CCATCAGAAG ATTTAGGTGT GTGCAGACAT GACCACACTC CCGTAGCAC TCCATAGCC 1674

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ala Ala Arg Pro Gly Leu Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1 5 10 15

Val Leu Gly Gly Gly His Leu Ser His Pro Pro His Val Phe Pro Gln
 20 25 30

Arg Arg Leu Gly Val Arg Glu Pro Arg Asp Met Gln Arg Glu Ile Arg
 35 40 45

Glu Val Leu Gly Leu Ala Gly Arg Pro Arg Ser Arg Ala Pro Val Gly
 50 55 60

Ala Ala Gln Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr
 65 70 75 80

Arg Ala Met Thr Asp Asp Ser Gly Gly Gly Thr Pro Gln Pro His Leu

- 82 -

85	90	95
Asp Arg Ala Asp Leu Ile Met Ser Phe Val Asn Ile Val Glu Arg Asp 100 105 110		
Arg Thr Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp 115 120 125		
Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg 130 135 140		
Ile Tyr Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile 145 150 155 160		
Ser Met Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu 165 170 175		
Phe Phe Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu 180 185 190		
Val Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His 195 200 205		
Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser 210 215 220		
Ile Asp Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser 225 230 235 240		
Arg Gln Pro Phe Met Val Gly Phe Phe Arg Ala Asn Gln Ser Pro Val 245 250 255		
Arg Ala Pro Arg Thr Ala Arg Pro Leu Lys Lys Lys Gln Leu Asn Gln 260 265 270		
Ile Asn Gln Leu Pro His Ser Asn Lys His Leu Gly Ile Leu Asp Asp 275 280 285		
Gly His Gly Ser His Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr 290 295 300		
Val Ser Phe Arg Asp Leu Gly Trp Leu Asp Ser Val Ile Ala Pro Gln 305 310 315 320		
Gly Tyr Ser Ala Tyr Tyr Cys Ala Gly Glu Cys Ile Tyr Pro Leu Asn 325 330 335		
Ser Cys Met Asn Ser Thr Asn His Ala Thr Met Gln Ala Leu Val His 340 345 350		
Leu Met Lys Pro Asp Ile Ile Pro Lys Val Cys Cys Val Pro Thr Glu 355 360 365		
Leu Ser Ala Ile Ser Leu Leu Tyr Tyr Asp Arg Asn Asn Asn Val Ile 370 375 380		
Leu Arg Arg Glu Arg Asn Met Val Val Gln Ala Cys Gly Cys His 385 390 395		

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- 83 -

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: /note= "BMP3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

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Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
1           5           10           15
Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser Gly
20           25           30
Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
35           40           45
Thr Ile Gln Ser Ile Val Ala Arg Ala Val Gly Val Val Pro Gly Ile
50           55           60
Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
65           70           75           80
Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
85           90           95
Thr Val Glu Ser Cys Ala Cys Arg
100

```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1           5           10           15
Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
20           25           30

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- 84 -

Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ser Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
 20 25 30
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Trp Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1247 base pairs
- (B) TYPE: nucleic acid

- 85 -

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS
(F) TISSUE TYPE: BRAIN

(ix) FEATURE:

(A) NAME/KEY: CIS
(B) LOCATION: 34..1199
(C) OTHER INFORMATION: /product= "GDF-1"
/note= "GDF-1 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

GGGGACACCG GCGCGGCGCT CAGCGCCACTG GTCCCGGGCG GCGGCGGACC CTGCGGCACTG      60
TCTGTGTCATG GCGTGGGAGG AAG ATG CCA CCG CCG CAG CAA GGT CCC TGC      110
                Met Pro Pro Pro Gln Gln Gly Pro Cys
                1                      5

GGC CAC CAC CTC CTC CTC CTC CTC GGC CTG CTG CTG CCC TCG CTG CCC      158
Gly His His Leu Leu Leu Leu Leu Ala Leu Leu Leu Pro Ser Leu Pro
10                      15                      20                      25

CTG ACC CCG CCC CCC GTG CCC CCA GGC CCA GGC GCG GCG CTG CTC CAG      206
Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu Gln
                30                      35                      40

GCT CTA GGA CTG CGC GAT GAG CCC CAG GGT GCG CCC AGG CTC CGG CCG      254
Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu Arg Pro
                45                      50                      55

GTT CCC CCG CTC ATG TGG CGC CTG TTT CGA CGT CGG GAC CCC CAG GAG      302
Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp Pro Gln Glu
                60                      65                      70

ACC AGG TCT GGC TCG CGG CCG ACC TCT CCA GGG GTC ACC CTG CAA CCG      350
Thr Arg Ser Gly Ser Arg Arg Thr Ser Pro Gly Val Thr Leu Gln Pro
                75                      80                      85

TGC CAC GTG GAG GAG CTC GGG GTC GCG GGA AAC ATC GTG CGC CAC ATC      398
Cys His Val Glu Glu Leu Gly Val Ala Gly Asn Ile Val Arg His Ile
                90                      95                      100                      105

CGG GAC CGC GGT GCG CCC ACC CGG GCG TCG GAG CCT GTC TCG GCC GCG      446
Pro Asp Arg Gly Ala Pro Thr Arg Ala Ser Glu Pro Val Ser Ala Ala
                110                      115                      120

GGG CAT TGC CCT GAG TGG ACA GTG GTC TTC GAG CTG TCG GCT GTG GAA      494
Gly His Cys Pro Glu Trp Thr Val Val Phe Asp Leu Ser Ala Val Glu
                125                      130                      135

CCC GCT GAG GCG CCG AGC CCG GCG CCG CTG GAG CTG CCT TTC GCG GCG      542
Pro Ala Glu Arg Pro Ser Arg Ala Arg Leu Glu Leu Arg Phe Ala Ala
                140                      145                      150

GCG GCG GCG GGA GCG CCG GAG GCG GCG TGG GAG CTG ACC GTG GCG CAA      590
Ala Ala Ala Ala Ala Pro Glu Gly Gly Trp Glu Leu Ser Val Ala Gln
                155                      160                      165

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- 86 -

GCG GGC CAG GGC GCG GGC GGC GAC CCC GGG CCG GTG CTG CTC CCG CAG Ala Gly Gln Gly Ala Gly Ala Asp Pro Gly Pro Val Leu Leu Arg Gln 170 175 180 185	638
TTG GTG CCG GGC CTG GGG CCG CCA GTG CCG GAG GAG CTG CTG GGC GGC Leu Val Pro Ala Leu Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala 190 195 200	686
GCT TGG GCT CCG AAC GCG TCA TGG CCG CCG AGC CTC CCG CTG GCG CTG Ala Trp Ala Arg Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu 205 210 215	734
GCG CTA CCG CCG CCG GCG CCG GCG GCG TCG CCG CCG CTG GCG GAG GCG Ala Leu Arg Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala 220 225 230	782
TGG CTG CTG CTG CTG AGC CTC GAC CCG CCG CTG TCG CAG CCG CTG GCG Ser Leu Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala 235 240 245	830
CGG CCG CCG CCG GAC CCG GAA CCG CTG TTG GCG GCG GCG CCG GCG GCG Arg Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly 250 255 260 265	878
GCT TGT CCG GCG CCG CCG CTG TAC GTG AGC TTC CCG GAG GTG GCG TGG Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp 270 275 280	926
CAC CCG TGG GTG ATC GCG CCG CCG GCG TTG CTG GCG AAC TAA TGG CAG His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln 285 290 295	974
GGT CAG TGG GCG CTG CCG GTC GCG CTG TCG GCG TCG GCG GCG CCG CCG Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro 300 305 310	1022
GCG CTC AAC CAC GCT GTG CTG CCG GCG CTG ATG CAC GCG GCG GCG CCG Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro 315 320 325	1070
GGA GCC GCG GAC CTG CCG TGC TCG GTG CCG GCG CCG CTG TCG CCG ATC Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala Arg Leu Ser Pro Ile 330 335 340 345	1118
TCC GTG CTC TTC TTT GAC AAC AGC GAC AAC GTG GTG CTG CCG CAG TAT Ser Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val Leu Arg Gln Tyr 350 355 360	1166
GAG GAC ATG GTG GTG GAC GAG TGC GCG TGC CCG TAA CCG GCG CCG GCG Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg 365 370	1219
CCCGGGCCCCA ACAATAAATG CCGCGTGG	1247

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- 87 -

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Pro Pro Pro Gln Gln Gly Pro Cys Gly His His Leu Leu Leu Leu
 1 5 10 15
 Leu Ala Leu Leu Leu Pro Ser Leu Pro Leu Thr Arg Ala Pro Val Pro
 20 25 30
 Pro Gly Pro Ala Ala Ala Leu Leu Gln Ala Leu Gly Leu Arg Asp Glu
 35 40 45
 Pro Gln Gly Ala Pro Arg Leu Arg Pro Val Pro Pro Val Met Trp Arg
 50 55 60
 Leu Phe Arg Arg Arg Asp Pro Gln Glu Thr Arg Ser Gly Ser Arg Arg
 65 70 75 80
 Thr Ser Pro Gly Val Thr Leu Gln Pro Cys His Val Glu Glu Leu Gly
 85 90 95
 Val Ala Gly Asn Ile Val Arg His Ile Pro Asp Arg Gly Ala Pro Thr
 100 105 110
 Arg Ala Ser Glu Pro Val Ser Ala Ala Gly His Cys Pro Glu Trp Thr
 115 120 125
 Val Val Phe Asp Leu Ser Ala Val Glu Pro Ala Glu Arg Pro Ser Arg
 130 135 140
 Ala Arg Leu Glu Leu Arg Phe Ala Ala Ala Ala Ala Ala Pro Glu
 145 150 155 160
 Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly Ala
 165 170 175
 Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu Gly Pro
 180 185 190
 Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg Asn Ala Ser
 195 200 205
 Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg Pro Arg Ala Pro
 210 215 220
 Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu Leu Val Thr Leu
 225 230 235 240
 Asp Pro Arg Leu Cys His Pro Leu Ala Arg Pro Arg Arg Asp Ala Glu
 245 250 255
 Pro Val Leu Gly Gly Gly Pro Gly Gly Ala Cys Arg Ala Arg Arg Leu
 260 265 270
 Tyr Val Ser Phe Arg Glu Val Gly Trp His Arg Trp Val Ile Ala Pro
 275 280 285
 Arg Gly Phe Leu Ala Asn Tyr Cys Gln Gly Gln Cys Ala Leu Pro Val
 290 295 300
 Ala Leu Ser Gly Ser Gly Gly Pro Pro Ala Leu Asn His Ala Val Leu
 305 310 315 320

- 88 -

Arg Ala Leu Met His Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys
325 330
Cys Val Pro Ala Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn
340 345 350
Ser Asp Asn Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu
355 360 365
Cys Gly Cys Arg
370